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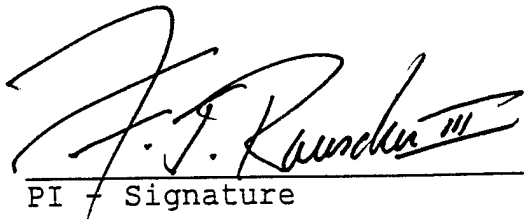
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**CHARACTERIZATION OF TWO PROTEINS WHICH INTERACT WITH THE  
BRACA1 GENE**

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## Introduction

The cloning of the chromosome 17q21 *BRCA1* breast cancer susceptibility gene is a landmark accomplishment in cancer genetics (Miki et al., 1994). Germline mutations in *BRCA1* appear to account for ~50% of familial breast cancers and essentially all families with 17q21-linked inherited susceptibility to ovarian and breast cancer (Szabo and King, 1995). The importance of this gene is underscored by the fact that kindreds segregating constitutive *BRCA1* mutations show a lifetime risk of 40-50% for ovarian cancer and >80% for breast cancer (Easton et al., 1993; Easton et al., 1995). The classification of *BRCA1* as a highly penetrant, autosomal dominant tumor suppressor gene has been genetically confirmed by the finding of frequent LOH of the wild-type allele in breast tumors from mutation carriers (Hall et al., 1990; Miki et al., 1994; Smith et al., 1992). Surprisingly, *BRCA1* mutations in sporadic breast cancer including those which show LOH have yet to be found and are extremely rare in sporadic ovarian cancer (Futreal et al., 1994; Merajver et al., 1995).

The *BRCA1* locus spans >100 kb comprising 24 exons (Miki et al., 1994). More than 100 constitutional mutations have been identified in *BRCA1* over the entire length of the gene and some clustering in populations and genotype-phenotype correlations have been suggested (FitzGerald et al., 1996; Ford et al., 1994; Muto et al., 1996; Roa et al., 1996; Struwing et al., 1995). The majority of germline mutations result in a truncated *BRCA1* protein although recurrent missense mutations resulting in amino acid substitutions in kindreds have also been observed (Couch and Weber, 1996). The heterogeneity of *BRCA1* mutant proteins produced by this spectrum of genetic mutations suggests that multiple, independent functions and/or protein-protein interaction surfaces are targets for mutational inactivation. However, the biochemical functions of *BRCA1* are largely unknown.

The predominant *BRCA1* mRNA of 8.0 kb encodes a 1863 amino acid protein with few sequence motifs suggestive of function (Miki et al., 1994). The most highly conserved regions are 1) the 100 amino acid N-terminus which encodes a RING finger motif which is predicted to bind zinc and may be a protein-protein interaction motif (Borden et al., 1995; Lovering et al., 1993); and 2) the C-terminus which contains an acidic region and a two copies of a novel motif, designated the BRCT domain, which is present in a variety of putative cell-cycle related proteins, including RAD9 and 53BP1 (Koonin et al., 1996). The most abundant *BRCA1* protein is now accepted to be a ~220 kDa phosphoprotein which is predominantly, but apparently not exclusively, nuclear in subcellular distribution (Chen et al., 1995; Chen et al., 1996; Scully et al., 1996). Other isoforms of *BRCA1* have been detected including a protein of 97 kDa which lacks exon 11, and thus a functional nuclear localization signal, and which is presumably the result of an alternative splicing event (Thakur et al., 1997). *BRCA1* is localized to discrete nuclear dot structures in a cell-cycle dependent manner (Scully et al., 1997). These observations, coupled with the finding of a transcriptional activation domain in the *BRCA1* C-terminus (Chapman and Verma, 1996) and the co-fractionation of *BRCA1* with the RNA pol II holoenzyme (Scully et al., 1997) suggest a role in transcriptional regulation.

The expression patterns of *BRCA1* further support its role in growth regulation and/or differentiation. The spatial-temporal expression pattern in the embryonic

mouse includes the neuroepithelium, and epithelial lineages of the skin, kidney and mammary gland (Marquis et al., 1995). Moreover, BRCA1 mRNA is sharply increased in alveolar and ductal cells of the breast epithelia during pregnancy (Marquis et al., 1995). Consistent with this, BRCA1 transcription is under (indirect) hormonal control in both cell culture and organismal systems (Gudas et al., 1995, 1996; Vaughn et al., 1996; Marks et al., 1997). BRCA1 is also highly expressed in the adult testis during the final stages of meiosis and spermiogenesis (Zabludoff et al., 1996). Together, these observations suggest a broad role for BRCA1 in terminal differentiation events in multiple tissues. Somewhat paradoxically, the murine *brca1*  $-/-$  embryos die very early in gestation and exhibit severe cell proliferation defects and profound cell cycle arrest (Hakem et al., 1996; Liu et al., 1996). The association of BRCA1 expression with both proliferation and differentiation events suggests a possible role for BRCA1 in regulating a genetic program which prepares the cell for terminal differentiation and possibly maintains that phenotype thereafter. Results of cell culture and transfection studies have further underscored the tumor suppression function of BRCA1 without revealing much of that mechanism. BRCA1 antisense expression can transform fibroblasts and accelerates growth of breast cancer cell lines (Rao et al., 1996; Thompson et al., 1995). Expression of wild-type *BRCA1* inhibits colony function and tumor growth *in vivo*, whereas tumor derived mutations of *BRCA1* abolish this growth suppression (Holt et al., 1996).

Evidence of a role for BRCA1 as a terminal differentiation checkpoint has recently been provided by the finding that BRCA1 and the RAD51 protein (involved in DNA recombination/repair) are co-localized and physically associated in mitotic and meiotic cells (Scully et al., 1997). The co-localization of BRCA1 and RAD51 on synaptonemal meiotic chromosomes suggests a role for this complex in either the fidelity of DNA replication, cell cycle progression or genomic integrity. Though intriguing, these results do not suggest a function for BRCA1 which is lost in tumor-derived mutations in BRCA1. Strategies based upon identification of proteins which bind to BRCA1 have yielded components of the nuclear import pathway (Chen et al., 1996) and a novel RING finger/BRCT-domain-containing protein, BARD1 (Wu et al., 1996). However, none of these associated proteins have suggested a function for BRCA1.

We have chosen to focus upon the highly conserved BRCA1 RING finger domain as a potential protein-protein interface. This motif is defined by a spatially conserved set of cysteine-histidine residues of the form C<sub>3</sub>HC<sub>4</sub>. Structural analysis of the motif shows that two molecules of zinc are chelated by the consensus residues in a unique "cross-braced" fashion (for reviews, see; Klug and Schwabe, 1995; Saurin et al., 1996). Comparative structure analyses suggest that the RING fingers have a common hydrophobic core structure but that the region encoded by amino acids spanning cysteines 24 and 64 (for BRCA1) forms a highly variable loop structure which is the determinant of protein-protein interaction specificity. The RING motif occurs in over 80 proteins including the products of a number of proto-oncogenes and putative transcription factors (Saurin et al., 1996). Evidence that the RING finger domain functions as a protein-protein interface has come from the study of the proto-oncogene PML (Borden et al., 1995) and the transcriptional co-repressor KAP-1 (Friedman et al., 1996). Intriguingly, like BRCA1, both PML and KAP-1 are localized to discrete, non-overlapping, nuclear dot structures and mutations in the RING finger of PML abolish its localization to the nucleus (Borden et al., 1995).

We hypothesize that the BRCA1 RING finger is a binding site for protein(s) which either mediate BRCA1 tumor suppressor function or serve to regulate these functions. Genetic evidence supports this in that single amino-acid substitutions at metal chelating cysteines, C61G and C64G, occur in kindreds; these mutations segregate with the disease susceptibility phenotype and are predicted to abolish RING finger structure. We have used the yeast two-hybrid system to isolate proteins which directly bind to the wild-type BRCA1 RING finger but not to the C61G or C64G mutated RING fingers or other closely related RING fingers. We have isolated mouse and human clones of a novel protein, BRCA1 associated protein-1 (BAP1), which fulfills all of these criteria. BAP1 is a novel, nuclear localized, enzyme which displays the signature motifs and activities of a ubiquitin carboxy-terminal hydrolase. Full-length BRCA1 binds to BAP1 *in vitro* and *in vivo* and BAP1 enhances the growth suppression properties of BRCA1 in colony formation assays. The human *BAP1* locus was mapped to chromosome 3p21.3 and homozygous deletions of *BAP1* were found in non-small cell lung cancers. Together, these data suggest that *BAP1* is a key player in the *BRCA1* growth suppression pathway and may itself be a tumor suppressor gene. The identification of BAP1 as a ubiquitin hydrolase implicates the ubiquitin-proteasome pathway in either the regulation, or as a direct effector, of BRCA1 function. BAP1 is the first nuclear-localized ubiquitin carboxy-terminal hydrolase to be identified and may play a broad role in ubiquitin-dependent regulatory processes within the nucleus, including the emerging role of ubiquitin conjugation as a subcellular targeting signal.

## BODY

### I. Experimental Methods

**Cell Culture, Transfections and Colony Formation Assays:** COS1 and HEP2 cells were grown at 37°C, 5% CO<sub>2</sub> in DMEM supplemented with 10% fetal bovine serum (FBS) and 2 mM L-glutamine. COS1 and HEP2 cells were transfected using DOSPOR transfection reagent (Boehringer Mannheim Biochemicals) following the manufacturers protocol. MCF7 cells were grown at 37°C, 5% CO<sub>2</sub> in DMEM supplemented with 10% FBS and non-essential amino acids.

**Colony Formation Assay:** MCF7 cells were transfected by a modified CaPO<sub>4</sub>-DNA precipitation method (Holt et al., 1996). MCF7 cells, at 2X10<sup>6</sup> cells/ 10 cm dish, were fed fresh medium approx. 3 hours prior to transfection and were then treated with the Ca-DNA precipitation. for 4 hours. The cells were subjected to a brief shock with transfection buffer containing 15% glycerol. Twelve to sixteen hours later, the cells were trypsinized, counted and plated directly into complete medium containing 0.75 mg/mL G418 at 5X10<sup>5</sup> cells per 10 cm dish. Cells were fed fresh medium containing G418 every three to four days. Cells were stained for colonies approximately 21 to 28 days after transfection.

**Yeast 2-hybrid:** The yeast 2-hybrid system as modified by Stan Hollenberg was used for all yeast experiments (Vojtek et al., 1993). Two libraries were screened for interaction with LexA-BRCA1; a human B cell, oligo-dT-primed, cDNA library [(Durfee et al., 1993); a kind gift of Dr. Steve Elledge] and a mouse embryo (9.5-10.5 day), random-primed, cDNA library size selected for inserts of 300 to 500 base pairs in length [(Vojtek et al., 1993); a kind gift of Dr. Stan Hollenberg].

**Construction of expression plasmids:**

**LexA fusion constructs:** The first 100 amino acids of human BRCA1 (BRCA1-RF) was used as the "bait" to screen for interacting proteins. The BRCA1-RF domain was made from overlapping oligonucleotides whose sequence had been optimized for expression in *E. coli* and *S. cerevisiae* (Madden, 1991 #44). Double-stranded DNA was generated by the polymerase chain reaction (PCR) and amplified with "outside" primers containing EcoRI and Sall enzymatic restriction sites (BRCA1-RF-5' oligonucleotide 5'-GCTAGAATTCACCATGGACCTGTCTGCTCTG-3'; BRCA1-RF-3' oligonucleotide 5'-GCTAGTCGACTTCCAGACCAGTGTCCAG-3'). A "wild-type" BRCA1-RF domain was confirmed by sequencing. The BRCA1-RF domain point mutants, BRCA1-C64G (Cys 64 to Gly) and BRCA1-C61G (Cys 61 to Gly), were created by PCR-mutagenesis using the "outside" primers described above and overlapping oligonucleotides containing the appropriate nucleotide change (BRCA1-C61G-sense 5'-CCATCTCAAGGTCCACTGTGTAAG-3'; BRCA1-C61G-antisense 5'-CTTACACAGTGGACCTTGAGATGG-3'; BRCA1-C64G-sense 5'-CAATGTCCAC TGGGTAAGAACG ACATC-3'; BRCA1-C64G-antisense 5'-GATGTGCTTCTT ACCCAGTGGACATTG-3'; Ho et al., 1989). The BRCA1-delAG185 mutant was generated by PCR using the BRCA1-RF-5' oligonucleotide and a 3' oligonucleotide that encoded the changed amino acid sequence (5'-GCATGGATCCTCAAACCTTGT GCAGGCAGGTACCCTGGTCAACAGGAGACAGGTGGGAAACCAGGATCTTTTGCATA GC-3'). The BRCA1-del31 truncation mutant was a mis-primed PCR reaction of



BRCA1-RF identified by sequencing. All LexA fusion constructs (wild-type and mutant) were made by cloning the appropriate BRCA1-RF domain into the vector pBTM-116 (Vojtek et al., 1993). The LexA-RPT-1 construct (amino acids 1-100) was made by PCR-mediated amplification of the corresponding nucleotides of a RPT-1 PCR sample [(Patarca et al., 1988); kindly provided by Dr. Harvey Cantor] followed by enzymatic digestion and ligation into the pBTM-116 vector. All clones were confirmed by sequencing. Expression of all constructs in yeast was confirmed by Western analysis using antibodies against the LexA DNA-binding domain (data not shown).

**BAP1 constructs:** A partial BAP1 cDNA (EST-BAP1) is encoded by two overlapping EST clones which were obtained from the Image Consortium [I.M.A.G.E. Consortium (LLNL) cDNA Clones #46154 and #40642; (Lennon et al., 1996)]. This partial BAP1 clone was generated by digesting clone #40642 with HindIII and FspI and clone #46154 with FspI and EcoRI. These two pieces were then ligated into the HindIII and EcoRI sites of the vector pcDNA3 (Invitrogen). Reverse-transcriptase-PCR using a gene-specific primer (5'-GAAGCGGATGTCGTGGTAGG-3') was used to identify 62 nucleotides which were missing from the "EST-BAP1" cDNA. These 62 nucleotides were inserted into the "EST-BAP1" cDNA by digestion of the RT-PCR product with the restriction enzymes KpnI (a unique site within the 5' RT-PCR oligonucleotide; 5'-CCTGTTATTAACCCTCACTAAAGGGAAGGGTACCATGAA TAAGGGCTGGCTGGAGC-3'; 3' RT-PCR-oligonucleotide 5'-GAAGCGGATGTCGTGGT AGG-3') and AvrII followed by ligation with AvrII+EcoRI digested "EST-BAP1" cDNA into KpnI-EcoRI digested pcDNA3. GST-hBAP1(483-729) was generated by cloning nucleotides 1486 to 3525 (the original two-hybrid clone) into pGEX-5x-1 (Pharmacia Biotech, Inc.). GST-hBAP1(438-594) and pACT-hBAP1(438-594) {nucleotides 1486-1821} were generated and amplified by PCR (pACT 5'-vector primer 5'-GATGTATATAACTATCTATTCG-3'; BAP1-*trunc.* oligonucleotide 5'-GCATAGATCTT CACCCCTGGCTGCCTTGGATTGG-3'), digested with restriction enzymes and ligated into the appropriate vector.

**Mapping of BRCA1/BAP1 interaction domain:** Truncations of mBAP1(596-721) were performed by PCR-based mutagenesis. The appropriate region of mBAP1(596-721) was amplified by PCR using a vector primer (pVP16 5'-primer, 5'-CCGATGCCCTT GGAATTGACGAG-3'; pVP16 3'-primer, 5'-CGATGAATTCTGAGCTAGCTTCTATC-3') and the appropriate truncating oligonucleotide (Mc43Ct1, 5'-GCATGAATTCTCAGCT CCGGCGCACTGAGATG-3'; Mc43Ct2, 5'-GCATGAATTCTCAAGCCAGCATGGA TATGAAGG-3'; Mc43Ct3, 5'-GCATGAATTCTCAGTCATCAATCTTGAAGTTC-3'; Mc43Ct4, 5'-GCATGAATTCTCATGCAATCTCGGCTTCTAC-3'; Mc43Nt1, 5'-GCATG GATCCCCAAGATTGATGACCAGCGAAGG-3'). The product was then ligated into the mouse library-yeast expression vector, pVP16. The point mutant mBAP1(L691P) was made by standard PCR-based mutagenesis protocols (Mc43(L691P) sense-primer, 5'-GCTGGCCCAACCCGGTGGAACAG-3'; Mc43(L691P) antisense-primer, 5'-CTGTT CCACCGGGTTGGCCAGC-3'; Ho et al., 1989) using the same vector primers described above. All clones were confirmed by sequencing and expression in yeast was confirmed by Western analysis using antibodies against the VP16 activation domain (data not shown).

**Tissue Northern:** Tissue RNA blots were obtained from Clontech Laboratories, Inc. (Palo Alto, CA). Blots were hybridized with  $^{32}\text{P}$ -labeled hBAP1(483-729) cDNA (nucleotides 1486 to 3525) using standard protocols.

**Fluorescent *In Situ* Hybridization (FISH):** FISH using a biotin-labeled 3.5 kb cDNA (full-length) clone of BAP1, with corresponding DAPI-banding and measurement of the relative distance from the short arm telomere to the signals (FLpter value) was performed as described previously (Tommerup and Vissing, 1995).

**Immunolocalization:** All immunofluorescence was performed as previously described (Ishov and Maul, 1996). BAP1 polyclonal antibodies were detected with FITC using biotin-avidin enhancement. Cells were stained for DNA with bis-benzimide (Hoechst 33258, Sigma Chemical Co.) and mounted using Fluoromount G (Fisher Scientific). Analysis was performed with a confocal scanning microscope (Leica, Inc.).

#### BAP1 Protein Characterization:

**Generation of antibodies:** Using PCR cloning (pACT 5'-vector primer 5'-GATGTATATAACTATCTATTTCG-3'; BAP1(antibody) 5'-CGTAGTCGAC TGTCAGCGCCAGGGGACTC-3'), the cDNA region encoding amino acids 483 to 576 of BAP1 was fused downstream of the 6 Histidine residues of the vector pQE-30 (QIAGEN Inc.). The His-tagged protein was purified from *E. coli* over a Ni-agarose column as previously described (Friedman, 1996 #76) and was used to immunize rabbits for the production of polyclonal antibodies (Cocalico Biologicals, Inc.). Immunoprecipitation of BAP1 was performed by previously described procedures for the metabolic labeling and immunoprecipitation of proteins from cell lysates (Friedman, 1996 #76).

***In Vitro* Protein Association:** GST, GST-hBAP1(483-729) and GST-hBAP1(483-594) were expressed in *E. coli* and then purified as described (Frangioni and Neel, 1993). The  $^{35}\text{S}$ -LexA-BRCA1-RF and  $^{35}\text{S}$ -BRCA1 were produced *in vitro* via coupled transcription/translation (TNT®, Promega Corp.). Association between proteins was assayed as described by Barlev et al. (1995).

**BAP1 Enzymatic Assay:** Assays for BAP1 enzymatic activity were performed essentially as described for the UCH-L1 and UCH-L3 enzymes (Mayer and Wilkinson, 1989). Briefly, bacteria (DH5a) harboring an IPTG-inducible expression plasmid containing BAP1 (pQE-30; QIAGEN Inc.) were grown and induced with 1 mM IPTG for 4 hours. The bacteria were collected and the pellets were resuspended to 1/20 volume (original culture) in lysate buffer (50 mM Tris, pH 8.0, 25 mM EDTA, 10 mM 2-mercapto-ethanol, 100 µg/ml lysozyme). The lysates were sonicated and centrifuged at 40,000 Xg. The soluble fractions were used for subsequent activity assays. The pellets were resuspended in an volume equal to that of the supernatant and samples of both pellet and supernatant were analyzed by SDS-PAGE for expression levels and inclusion body formation.

Assays for ubiquitin carboxy-terminal hydrolase activity were performed using the glycine 76 ethyl ester of ubiquitin (Ub-OEt) as a substrate (Mayer and Wilkinson, 1989; Wilkinson et al., 1986). Assay reactions (20 µL) contained 3.0 µg Ub-OEt and sample enzyme in assay buffer (50 mM Tris pH 7.6, 100 µg/ml Ovalbumin, 10 mM DTT), and

were incubated at 37°C for 10 min. Reactions were stopped by addition of 80 µl of the HPLC solvent followed by refrigeration. Ester hydrolysis was detected by C8 reverse phase HPLC with isocratic 45% acetonitrile in 50 mM perchlorate (pH 2) as solvent. Assays were done in triplicate. The peak areas were integrated and normalized with respect to a ubiquitin standard.

#### Mutation Screening:

RNA/DNA Preparation: Genomic DNA was prepared from breast and lung cancer cell lines using standard methods. Total RNA was extracted by the cesium chloride-ultracentrifugation method (Ausubel et al., 1987). First strand cDNAs were synthesized from RNA by M-MLV reverse transcriptase (Gibco BRL) according to the manufacturer's instructions.

Southern and Northern Blot Hybridization: Five µg of genomic DNA, subjected to restriction enzyme digestion, or ten µg total RNA, was electrophoretically gel-fractionated and transferred to Hybond N+ membranes (Amersham). Hybridization was performed with a radiolabeled full-length BAP1 cDNA probe followed by washes under standard conditions and detection by autoradiography.

Single Strand Conformational Polymorphism (SSCP) Analysis: Seventeen overlapping PCR primer pairs, each with a predicted product size of approximately 200 base pairs, were designed to span the 2.2 kb open reading frame of the BAP1 cDNA sequence. One µl cDNA (from RNA) was then amplified in 20 µl PCR reactions containing 20 mM Tris HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl, 0.2 mM each dNTP, 0.1 mM each forward and reverse primer, 0.05 ml <sup>32</sup>P-α dCTP, and 0.5 units Taq DNA Polymerase (BRL). PCR reactions were carried out in a Perkin-Elmer 9600 Thermocycler using a touchdown technique: a 2.5 min. initial denaturation at 94°C was followed by 35 cycles of denaturation at 94°C x 30s, annealing, initially at 65°C decreasing by 1°C for each of the first ten cycles to 55°C, x 30s, and extension at 72°C x 30s with a final extension of 5 min at 72°C. PCR products were then diluted 1:10 with SSCP dye (95% formamide, 20 mM EDTA, and 0.05% each of bromophenol blue and xylene cyanol), heat-denatured, and electrophoresed on 0.5X MDE gels +/- 10% glycerol. Abnormal single-stranded DNA detected as autoradiographic shifts were reamplified by PCR and subjected to automated dye-terminator sequencing (ABI 373).

## II. Results

### A Yeast Two-Hybrid Screen for BRCA1 RING Finger Interacting Proteins

The mouse and human BRCA1 RING finger regions are shown in Fig. 1A and are compared to related RING domains. The signature C<sub>3</sub>HC<sub>4</sub> structure is highlighted. The RING finger from the RPT-1, a putative lymphocyte-specific transcription factor, is most highly related to BRCA1 (Patarca et al., 1988). We constructed a totally synthetic BRCA1 gene encoding the amino-terminal 100 amino acids of human BRCA1 using long oligonucleotides and PCR-mediated overlap-extension gene synthesis techniques (Madden, 1991 #44). Codon usage was optimized for expression in *E. coli* and *S. cerevisiae*. The resulting gene was fused to the LexA DNA binding domain (Fig. 1B). The negative control/specificity controls included 1) the Cys61Gly and Cys64Gly substitutions of BRCA1 which occur in breast cancer pedigrees, 2) the protein equivalent of the del AG185 mutation which results in a frame shift at amino

acid 22 followed by 17 out-of-frame amino acids and a stop codon, 3) a truncated BRCA1 RING finger at amino acid 31, the result of a PCR error, 4) the RPT-1 RING finger domain, and 5) a non-specific control LexA fusion with RhoB. The wild-type BRCA1 RING finger (BRCA1-RF) did not display intrinsic transcriptional activation function in yeast and proper expression of each LexA fusion in yeast was confirmed by Western blot analysis (data not shown).

Guided by the expression patterns of BRCA1 during mouse development and in human spleen, we chose to screen cDNA libraries constructed from E9.5-10.5d whole mouse embryos and human adult B cells with the LexA-BRCA1-RF. Thirty-one cDNAs which specifically interacted with BRCA1-RF were obtained: 8 of these (3 from the human library and 5 from the mouse library) encoded the same amino acid sequence and were further pursued. Each clone shares the same translational reading frame with the transcriptional activation domain to which it is fused and in addition, the fusion junctions were different among the clones suggesting that the interaction was not due to a fusion-junction artifact. Fig. 2A shows a representative secondary screen for a subset of these clones performed by re-introducing the indicated purified plasmids into naive yeast. Each clone showed a strong interaction with the BRCA1-RF but failed to interact with the C64G, C61G (data not shown), del31, delAG (data not shown), RPT-1, RhoB, or any of the specificity control LexA fusions (data not shown). The longest cDNA retrieved in the two-hybrid screen was a ~2.0 kb clone from the human library and encoded 246 amino acids followed by a 1.3 kb 3'UTR. Each mouse clone encoded an overlapping smaller subset of this human open reading frame which served to partially map the minimal interaction domain. A more detailed analysis of the BRCA1/BAP1 interaction is discussed below and shown in Fig. 2B. Interestingly, the mBAP(518del718) clone interacted most poorly with BRCA1-RF and lacked a 93 bp sequence (the reading frame was maintained), possibly the result of a naturally occurring splice variant. That these clones fail to bind multiple, independent tumor-derived mutations of the BRCA1-RF provides strong genetic evidence for their relevance to the functions of BRCA1.

### Analysis of the BAP1 cDNA

We designated this gene product BRCA1 associated protein (BAP1): A nearly full-length cDNA was constructed via a combination of cDNA library screening, EST database searching, 5'RACE and RT-PCR (Fig. 3A). The current BAP1 cDNA comprises 3525 bp; a polyA tract is present along with multiple polyA signals. Conceptual translation yields a long open reading frame of 729 amino acids with a predicted MW of 81 kDa and pI of 6.3. The presumptive initiator methionine is within a favorable context for translation start, however the short 5'UTR of 39 bp encodes amino acids in-frame with the presumptive methionine and does not contain a stop codon. BLAST searches indicated that BAP1 is a novel protein with motifs suggestive of function. The amino-terminal 240 amino acids show significant homology to a class of thiol proteases, designated ubiquitin C-terminal hydrolase (UCH), which are implicated in the proteolytic processing of ubiquitin (Wilkinson et al., 1989). These enzymes play a key role in protein degradation via the ubiquitin-dependent proteasome pathway. The most closely related UCH is a hypothesized protein from *C. elegans* which shares 63% similarity (40% identity) with BAP1 through the UCH domain and is also likely to be a UCH enzyme (Figs. 3B and 3C). Pairwise similarities to other mammalian UCHs of 54% (UCHL3) and 56% (UCHL1) have also been found

(Figs. 3B and 3C). Most importantly, the residues which form the catalytic site (Q85, C91, H169, and D184) are completely conserved, including the FELDG motif (Larsen et al., 1996). In addition, a loop of highly variable sequence, which is disordered in the crystallographic structure of human UCH-L3 (Johnston et al., 1997), is present (residues 140 to 167). This loop may occlude the active site or provide substrate specificity for the enzyme.

BAP1 has a number of additional motifs; a region of extreme acidity spanning amino acids 396 to 408, as well as multiple potential phosphorylation sites and N-linked glycosylation sites (Figs. 3A and 3B; S. Subbiah, personal communication). The C-terminal one-third is highly charged and is rich in proline, serine and threonine. The extreme C-terminus contains two putative nuclear localization signals, KRKKFK and RRKRSR, and is hydrophilic; it is predicted to fold into a helical (possibly coiled-coil) structure (Figs. 3A and 3B). Indeed, definition of the BAP1-BRCA1 interaction by deletion mutagenesis supports this hypothesis. Deletion of protein sequence from the carboxy or amino termini of mBAP1(596-721) (the "minimal interaction domain") almost completely destroyed the BAP1-BRCA1 interaction (Fig. 2B). Furthermore, within the BAP1 minimal interaction domain, the mutation of leucine 691 to a proline, predicted to disrupt the helical nature of this region, disrupted the BAP1-BRCA1 interaction, consistent with the hypothesis that BAP1 uses a coiled-coil domain to interact with the RING finger domain of BRCA1. This overall architecture suggests that BAP1 may be a novel, nuclear-localized, member of the UCH enzyme family.

#### BAP1 is a 90 kDa Protein With UCH Activity

The BAP1 open reading frame encodes a protein of 81 kDa predicted molecular weight. Expression of the cDNA *in vitro* and analysis by SDS-PAGE yielded a single major protein with an apparent molecular weight of 90 kDa (Fig. 4A). Immunoprecipitation of this product with anti-BAP1 antiserum confirmed that the protein expressed *in vitro* resulted in a polypeptide that contained the antigen used to raise the antibody. Furthermore, expression of the BAP1 cDNA in COS1 cells followed by immunoprecipitation of <sup>35</sup>S-labeled whole cell extracts also yielded a protein with an apparent molecular weight of 90 kDa (Fig. 4A). The difference between apparent and predicted molecular weights may be accounted for by the unusual properties of the C-terminus or by post-translational modifications; however, this has yet to be determined.

To determine whether BAP1 did indeed have UCH activity, the BAP1 cDNA was expressed in bacteria and this protein was assayed for the ability to hydrolyze the glycine 76 ethyl ester of ubiquitin (Ub-OEt; Mayer and Wilkinson, 1989). Overexpression of BAP1 in bacteria led to abundant protein, most of which was found in an inactive, insoluble form (Fig. 4B, lower panel, compare uninduced and induced precipitates). The BAP1 protein found in the soluble fraction was able to hydrolyze Ub-OEt and the level of this activity increased with the level of protein (Fig. 4B, lower panel) indicating that BAP1 contains UCH-like enzymatic activity. The active site thiol residue responsible for UCH activity in UCH-L3 has been identified and its mutation leads to abolition of enzyme activity (Larsen et al., 1996). Mutation of the corresponding cysteine residue in BAP1, BAP1(C91S), yielded a protein with no UCH activity (Fig. 4C) further suggesting that BAP1 is a thiol protease of the UCH family.

### BAP1 Associates With BRCA1 *in vitro*

Association of the BRCA1-RF with BAP1 was confirmed *in vitro* by binding of <sup>35</sup>S-labeled LexA-BRCA1-RF to hBAP1(483-729) fused to glutathione S-transferase (GST; Fig. 5A). The labeled BRCA1-RF specifically bound to the GST-hBAP1(483-729) fusion protein, but not to GST alone (Fig. 5C) confirming a physical association of the two proteins. To confirm that the association of the BRCA1-RF to BAP1 was not an artifact of using only a portion of BRCA1, full-length BRCA1 was expressed *in vitro* and incubated with GST and GST-hBAP1(483-729) (Fig. 5B). As a further control for the specificity of the interaction, BRCA1 was also incubated with GST-hBAP1(483-594), a GST-BAP1 fusion protein lacking the minimal interaction domain (see Figs. 2A and 3). The BRCA1 protein specifically bound to GST-hBAP1(483-729) and not to GST or GST-hBAP1(483-594) (Fig. 5B), confirming the direct interaction of BRCA1 with BAP1 through the C-terminal region of BAP1.

### BAP1 is a Nuclear Protein Expressed in a Variety of Tissues

A direct interaction between BAP1 and BRCA1 suggests that BAP1 might be expressed in an overlapping subset of tissues expressing BRCA1 and that the subcellular location of BAP1 and BRCA1 may be the same. The expression of BAP1 in a variety of human adult tissues was determined by Northern blot analysis. Probing these blots with a 2.0 kbp radiolabeled partial BAP1 cDNA (nucleotides 1488 to 3525) indicated that the mRNA encoding BAP1 was present as a single mRNA species of ~4 kb in all tissues except testis, where a second, ~4.8 kb mRNA, was also detected (Fig. 6A). Highest expression was detected in testis, placenta and pancreas with varying levels detected in the remaining tissues. Expression of BAP1 in normal breast tissue was confirmed by RT-PCR of total RNA isolated from HMEC cells (data not shown). The level and pattern of tissue expression shown by BAP1 is similar to that shown by BRCA1 (Miki et al., 1994).

The location of BAP1 within the cell was determined by immunofluorescence microscopy. HEP2 epithelial cells were transfected with the BAP1 cDNA and analyzed by immunofluorescence staining with  $\alpha$ BAP1 antibodies. BAP1 was found almost exclusively in the nucleus of the cell (Fig. 6B; green staining of the two leftmost cells), consistent with 1) its association with BRCA1, and 2) the presence of 2 nuclear localization signals in the BAP1 protein sequence.

### BAP1 Augments the Growth Suppressive Activity of BRCA1

The biochemical function of BRCA1 is currently unknown, however, several studies have shown that BRCA1 can affect the growth characteristics of cells (Holt et al., 1996; Rao et al., 1996). To determine whether BAP1 may affect cell growth itself or may affect BRCA1-mediated changes in cell growth, BRCA1 and BAP1 cDNAs were co-transfected into MCF7 breast cancer cells (Fig. 7). This cell line was chosen for several reasons; one, it has been previously shown that these cells are inhibited by the overexpression of BRCA1 (Holt et al., 1996); two, both northern and RT/PCR analyses showed that BAP1 was expressed in this cell line (data not shown); and three, analysis of the open reading frame from BAP1 cDNA prepared from this cell line showed no mutations (data not shown).

The expression of BRCA1 alone (BRCA1:pCMV5) decreased the number of colonies formed by these cells when compared to the vector control (pcDNA3:pCMV5), in agreement with other studies (Holt et al., 1996). The co-expression of BRCA1 and BAP1 (BRCA1:BAP1) significantly decreased the number of cell colonies (approximately 4-fold vs. BRCA1 alone; see Fig. 7B) indicating that BAP1 enhances the growth suppressive actions of BRCA1. A mutant of BAP1, BAP1(165-729), in which the enzymatic region is deleted but which still binds to BRCA1 (data not shown), also enhanced the growth suppression of BRCA1, but not to the same extent as the wild-type BAP1.

In contrast to BRCA1, the expression of BRCA1-D11 (BRCA1 missing the 11th exon) in MCF7 cells by itself had no effect on the growth of MCF7 cells (Fig. 7). However, the co-expression of BRCA1-D11 and BAP1 significantly decreased the number of colonies, suggesting that the presence of BAP1 could functionally substitute for the missing 11th exon of BRCA1 and/or that BAP1 itself was an inhibitor of cell growth. In support of this latter hypothesis, the expression of BAP1 in MCF7 cells did somewhat reduce the number of colonies formed (pcDNA3:BAP1; see Fig. 7B). The expression of the enzymatic mutant, BAP1(165-729), alone or in combination with BRCA1-D11 yielded the same number of colonies. Thus, enzymatically active BAP1 enhances BRCA1-mediated suppression of growth.

BAP1 is Located on Chromosome 3p21.3 and is Mutated in Non-Small Cell Lung Carcinoma.

The possibility that BAP1 may be a tumor suppressor gene suggested that its deletion might play a critical role in tumor pathogenesis. We questioned whether BAP1 might be located at a chromosomal region routinely mutated in breast cancer. The full-length BAP1 cDNA was used in fluorescent *in situ* hybridization (FISH) to identify the chromosomal location of the *BAP1* gene (Fig. 8). Specific signals were observed only on the midportion of chromosome 3 with 42 of 69 analyzed metaphase spreads showing at least one specific signal. The FLpter value was  $0.27 \pm 0.02$ , corresponding to a localization for BAP1 at 3p21.1-p21.31. This location is a region of LOH for breast cancer as well as a region routinely deleted in lung carcinomas (Buchhagen et al., 1994; Thiberville et al., 1995).

The chromosomal location of *BAP1* suggested the possibility of mutations within *BAP1* in tumor samples. Thus, a variety of tumor samples were screened for mutations within the *BAP1* gene by Southern, Northern and PCR-based SSCP analyses. Genomic DNAs from a panel of small cell lung cancer (SCLC), non-small cell lung cancer (NSCLC), breast cancer, and lymphoblastoid cell lines, were subjected to EcoR1 digestion and then hybridized to a radio-labeled, full-length BAP1 probe. A single 23 kb band was detected in the lymphoblastoid and most tumor cell lines (data not shown). One NSCLC line, H226, did not show the 23 kb band but did show an aberrant approximately 30 kb band (data not shown; This finding was confirmed in a second experiment using freshly prepared genomic DNA from this cell line). To further characterize this potential genomic rearrangement, we subjected genomic DNA from H226 and a smaller number of lung cancer and lymphoblastoid lines to BamH1 digestion. Using the full-length BAP1 probe, we detected four distinct bands at 7.5 kb, 4.0 kb, 3.0 kb, and 2.4 kb which were present in all cell lines tested with the exception

of H226 (Fig. 9A). In the H226 line, we detected only the 2.4 kb band and an aberrant 2.6 kb band.

Further mutational analysis of BAP1 was performed by screening a panel of lung cancer and lymphoblastoid cell lines for expression of the BAP1 mRNA. Northern analysis showed that most cell lines expressed a single ~4 kb mRNA (Fig. 9B). However, two cell lines, H226 and H1466 (both NSCLCs), showed undetectable levels of BAP1 expression (a not unexpected result for sample H226) suggesting that BAP1 may play a critical role in NSCLC pathogenesis.

Finally, a panel of lung and breast cancer cell lines were screened for mutations in the BAP1 open reading frame by RTPCR-SSCP (Fig. 9C). We detected a homozygous 8 base pair deletion in the cDNA from the NSCLC line H1466. This short deletion leads to a frameshift and encodes a 393 amino acid protein. This homozygous deletion was confirmed to be present in genomic DNA from the same cell line. These data clearly show that genetic alterations, including intragenic homozygous deletions, occur in BAP1.

### III. Discussion:

We have discovered and characterized a novel protein, BAP1, which binds to the BRCA1 RING finger motif. A number of lines of evidence are offered which support a role for BAP1 in BRCA1 signal transduction pathways. Specifically, we showed that: 1) BAP1 binds to the RING finger of BRCA1, but not to tumor-derived mutants of BRCA1 or related RING domains; 2) The BAP1-BRCA1 interaction occurs *in vitro* and BAP1 mRNA is expressed in those tissues which also express BRCA1; 3) BAP1 is a nuclear-localized, ubiquitin carboxy-terminal hydrolase (UCH) which cleaves model ubiquitin substrates *in vitro*; 4) BAP1 enhances BRCA1-mediated suppression of cell growth in colony formation assays and does so in a manner dependent upon the UCH enzymatic domain and the BRCA1-interaction domain; and 5) Human BAP1 maps to 3p21.3 and intragenic, homozygous deletions occur in non-small cell lung cancer cell lines. Together, these observations suggest that BAP1 is a tumor suppressor gene and that it serves either as a regulator or an effector in BRCA1 growth control pathways. Both the specificity of the BRCA1 RING finger-BAP1 interaction and the fact that independent, tumor-derived missense mutations in the cysteines in the BRCA1 RING finger domain abolish interaction with BAP1 provide compelling evidence for the physiological relevance of this interaction.

Any discussion of mechanisms of BRCA1-BAP1 mediated growth control must center on the fact that BAP1 is a protease of the ubiquitin carboxy-terminal hydrolase (UCH) family. This discovery immediately implies a role for either ubiquitin-mediated, proteasome-dependent degradation or other ubiquitin-mediated regulatory (Isaksson et al., 1996) pathways in BRCA1 function. Regulated ubiquitination of proteins and subsequent proteasome-dependent proteolysis plays a role in almost every cellular growth, differentiation and homeostatic process (reviewed by Ciechanover, 1994; Isaksson et al., 1996; Wilkinson, 1995). This pathway can be broadly subdivided into reactions involving 1) pro-ubiquitin processing and ATP-dependent activation of ubiquitin; 2) substrate recognition, conjugation and editing of the polyubiquitin chain; 3) proteasome-dependent degradation of the ubiquitin protein and; 4) cleavage/debranching of peptide-ubiquitin conjugates and recycling of ubiquitin to



cellular pools. The pathway is regulated at almost every step. First, at the level of substrate specificity via the concerted actions of activating enzymes, carrier proteins and ligation enzymes, and secondly, at the level of proteolytic deubiquitination and ubiquitin hydrolysis. The latter enzymes are ubiquitin-specific thiol proteases which can be broadly classified into two families: the ubiquitin-specific proteases (UBPs) and the ubiquitin carboxy-terminal hydrolases (UCHs).

The UBP family members are 50-300 kDa, cytoplasmic or nuclear-localized proteins which, in general, cleave ubiquitin or ubiquitin-conjugates from large substrates. Such enzymatic activity can be found directly associated with the 26S proteasome and may serve a regulatory function by editing ubiquitin on large substrates or cleaving polyubiquitin, thus replenishing ubiquitin pools (Lam et al., 1997). Remarkably, a number of UBPs have been isolated as growth regulatory and/or developmental control genes such as DOA4 in yeast, which controls DNA replication and repair (Papa and Hochstrasser, 1993); UBP3 which is involved in transcriptional silencing in yeast (Moazed and Johnson, 1996); the TRE2 oncogene which is mutated in the UBP active site and functions as a dominant negative transforming gene (Nakamura et al., 1992); the drosophila *Fat Facets* gene which controls pattern formation and eye development (Huang et al., 1995; Huang and Fischer-Vize, 1996); and the human DUB family of cytokine-inducible UBPs which control hematopoietic differentiation (Zhu et al., 1996, 1997).

By contrast, the UCH family has been characterized as a set of small (25-30 kDa) cytoplasmic proteins which prefer to cleave ubiquitin from ubiquitin-conjugated small substrates and may also be involved in the co-translational processing of proubiquitin. Like the UBPs, UCHs show considerable tissue specificity and developmentally-timed regulation (Wilkinson et al., 1992). UCH family members are strongly and differentially expressed in neuronal, hematopoietic and germ cells in many species. Most remarkably, a novel UCH enzyme has recently been cloned from *Aplysia Californicus* whose enzymatic function is essential for acquisition and maintenance of long-term memory (Hedge et al., 1997). Finally, UCH levels are strongly down-regulated during viral transformation of fibroblasts (Honore et al., 1991), consistent with a role in growth control.

BAP1 is the newest member of the UCH family and considerably expands the potential roles of this family of proteases. BAP1 is a much larger protein (90 kDa) and is the first nuclear-localized UCH. In addition to containing the ~250 amino acid amino-terminal UCH catalytic domain, it includes a long carboxy-terminal extension with rich in proline, serine and threonine and a short, highly acidic region, elements which may confer a short half-life (Rechsteiner et al., 1996). The extreme carboxy-terminus encodes two potential nuclear localization signals which overlap the approximately 125 amino acid BRCA1 interaction domain. It was this domain that was independently isolated from mouse and human libraries in the two-hybrid screen and is predicted to fold into a long amphipathic helix of coiled-coil character, the structure of which may be important for BRCA1 interaction: Substitution of proline 691 with a leucine abolishes the BAP1-BRCA1 interaction. We have also detected a potential splice variant in BAP1 which results in loss of 31 amino acids of the BRCA1 interaction domain and greatly reduces the ability of BAP1 to bind the BRCA1 RING finger, further suggesting that the BAP1-BRCA1 interaction is regulated. Thus, our data suggest that

the BAP1 carboxy-terminus is tethered to BRCA1 via the RING finger domain and that the UCH catalytic domain is free to interact with ubiquitin substrates.

A simple model explaining most of our data is that BRCA1 is a direct substrate for the UCH activity of BAP1. Thus, in contrast to all of the known UCHs which are comprised entirely of the UCH domain, the carboxy-terminal extension provides substrate and/or targeting specificity for the catalytic function. Paradigms for separate substrate recognition and catalytic domains occur throughout the ubiquitin conjugation/ligation system (see Wilkinson, 1995 and references therein). Regulated ubiquitination of BRCA1 and subsequent proteasome-mediated degradation would not be surprising given that both BRCA1 levels and subnuclear localization are tightly regulated in the mitotic cell-cycle and during meiosis (Gudas et al., 1996; Scully et al., 1997; Zabludoff et al., 1996). BAP1-mediated deubiquitination of BRCA1 would be expected to stabilize the protein and protect it from proteasome-mediated degradation. This scenario is consistent with both the ability of co-transfected BAP1 to enhance the tumor suppressor effects of BRCA1 in colony formation assays and the finding of mutations in BAP1 in cancer cell lines.

A second, and equally plausible, hypothesis is that the BRCA1-BAP1 association serves to target the UCH domain to other substrates. These substrates may be bound to other sites on BRCA1; in this scenario, BRCA1 could be construed as an assembly or scaffold molecule for regulated assembly of multiprotein complexes, a function which has been postulated for other tumor suppressor proteins (e.g. pRb; Sellers and Kaelin, 1996; Welch and Wang, 1995). BAP1 could thus be a regulator of this assembly via controlled ubiquitin proteolysis. In this context, it is interesting to note that two other RING finger-containing proteins are involved in controlled proteolysis processes which depend upon the integrity of the RING finger structure: 1) the mouse homologue of the drosophila *seven-in-absentia* (a RING finger protein) binds to the tumor suppressor protein Deleted in Colon Cancer (DCC), thus targeting it for proteasome-mediated degradation. This degradation requires the RING finger structure (E. Fearon, personal communication). 2) The herpes virus protein VMW110 RING finger protein binds directly to a UBP family member, HAUSP, and appears to target it to the ND10/POD nuclear dot structure, which itself contains the RING finger-containing proto-oncogene PML (Everett et al., 1997).

In this context, it is interesting to note that BRCA1 is also localized in nuclear dot structures in a cell-cycle dependent manner (Scully et al., 1997). This association of BRCA1 with RAD51 in both mitotic and meiotic cells broadly implicates BRCA1 in DNA repair and/or recombination processes. The RAD51/52-dependent DNA repair pathway is highly regulated and includes many proteins, some of which may be potential substrates for BAP1-mediated ubiquitin hydrolysis. RAD23, which associates with the RAD51/52 complex contains an amino-terminal ubiquitin-like domain which is required for RAD23 function and double-strand break repair (Watkins et al., 1993). Recently, a human ubiquitin-like protein, UBL-1, was isolated as a protein which binds directly to the human RAD51/RAD52 complex (Shen et al., 1996). Interestingly, the yeast homologue of UBL1 is SMT3, which functionally associates with the yeast centromere protein MIF2, a protein required for proper chromosome segregation (Brown, 1995; Brown et al., 1993). It is possible that BAP1, which is co-expressed with BRCA1 in testis, may regulate the recombination/repair functions of the BRCA1/RAD52 complex by targeting either RAD23 or UBL1 for ubiquitin hydrolysis.

## Conclusions

We have identified a novel protein, BAP1, which binds to the BRCA1 RING finger domain (BRCA1-RF). BAP1 is a new, nuclear-localized, ubiquitin carboxyl-terminal hydrolase suggesting that deubiquitinating enzymes may play an important role in BRCA1 function. BAP1 binds to the wild-type BRCA1-RF both *in vitro* and *in vivo*, but not to mutant BRCA1-RF's found in tumors from breast cancer kindreds, or to related RING-finger proteins. BAP1 enhances BRCA1-mediated tumor suppression in colony formation assays and this activity requires the enzymatic function. BAP1 was mapped to human chromosome 3p21; rearrangements and intragenic mutations of BAP1 have been found in lung carcinomas, including a homozygous deletion. BAP1 is the first nuclear-localized ubiquitin carboxy-terminal hydrolase (of the UCH class) to be identified and may be a new tumor suppressor gene which functions in the BRCA1 growth control pathway.

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## Appendices

### Figures

**Figure 1** Structural features of the BRCA1 gene product. A) Alignment of the RING finger domains of human and mouse BRCA1 (AA's 21-67), RPT-1 (AA's 12-61; the most closely related RING finger) and BARD1 (AA's 47-89). Asterisks (\*) identify the Zn-chelating amino acids that form the core of the RING finger. Boxed amino acids show regions of identity between the RING finger domains of human BRCA1 and the other proteins. Alignment performed by ClustalW (Thompson et al., 1994). B) The amino-terminal 100 amino acids of human BRCA1 (which includes the RING finger domain) or the indicated amino acids of the various BRCA1-RF mutants and controls were fused to the LexA DNA-binding domain. Expression of all fusions in yeast were confirmed by Western analysis. The LexA-BRCA1 fusion protein was used in the yeast 2-hybrid screen to identify interacting proteins.

**Figure 2** Identification of the same BRCA1-RF-interacting protein from human and murine libraries that function in the yeast 2-hybrid system. A) The BRCA1-interacting protein specifically interacts with the BRCA1 RING finger domain. Two hybrid screens of a human B-cell library and a mouse embryo (9.5-10.5d) library identified a protein that interacted with wild-type BRCA1-RF, but not with BRCA1-del31 {a truncated BRCA1}, BRCA1(Cys64Gly) {a BRCA1-RF containing a point mutation}, RPT-1 {a RING finger closely resembling the BRCA1}, or RhoB {a non-related protein}. Dark color of yeast indicates transcription from the LacZ locus - a positive interaction. Clones obtained from the two libraries are described as partial BAP1 proteins with A.A.s in parentheses. h, human; m, mouse. B) BAP1 interaction requires its C-terminal domain. Murine clone mBAP1(596-721) defines the minimal interaction domain of BAP1. Mutants of this clone were generated by PCR-based deletion or point mutagenesis of mBAP1(596-721) as described in Materials and Methods. Each individual mutant was co-transformed with LexA-BRCA1-RF into L40 yeast and tested for interaction via its ability to activate transcription from the LacZ locus.

**Figure 3** BAP1 is a novel ubiquitin carboxy-terminal hydrolase (UCH). A) The nucleotide and amino acid sequence of BAP1. The longest open reading frame which contained the amino acids defined by the human 2-hybrid fusion protein is 2188 nucleotides encoding 729 amino acids. The cDNA also contains 39 nucleotides of 5'UTR and 1705 nucleotides of 3'UTR. The enzymatic active site is contained within the first 250 amino acids; the active site residues are circled. The putative nuclear localization signals (NLS) are underlined, the highly acidic region is boxed with heavy lines, the interaction domain is boxed and the protein fragment used to generate BAP1 polyclonal antibodies is bracketed (A.A.'s 483-576). B and C) Comparison of BAP1 with other UCH's. UCH-CAEEL (genebank # Q09444), UCH DROME (genebank # P35122), UCHL-1 (genebank # P09936), UCHL-3 (genebank # P15374). The BLAST search algorithm was used to identify proteins closely related to BAP1 (Altschul et al., 1990). The UCH domain of four of these proteins were aligned with BAP1 using the CLUSTALW (ver.1.6) algorithm (Thompson et al., 1994). Areas of homology with other UCH's are boxed. Only CAEEL-CO8B11.7 showed any homology outside of the enzymatic region. The region necessary for the interaction with BRCA1 (AAs 598-729) is indicated in the diagram with light crosshatching.

**Figure 4** Expression and enzymatic activity of the BAP1 Protein. A) BAP1 has an apparent molecular weight of 90 kDa. The BAP1 cDNA was transcribed and translated *in vitro* (BAP1 IVT) in the presence of <sup>35</sup>S-Methionine and immunoprecipitated with either pre-immune or anti-BAP1 sera. BAP1 was also immunoprecipitated from extracts of <sup>35</sup>S-labeled COS1 cells transfected with empty expression plasmid or with plasmid including the BAP1 cDNA. B) BAP1 has ubiquitin hydrolase activity. BAP1, or an enzymatically null mutant, BAP1(C91S), were expressed in bacteria by IPTG induction. Bacteria were harvested, lysed and supernatant and pellet fractions generated. Each fraction was then measured for UCH activity (bar diagram; n.d., not detected). Induction of protein was verified by SDS-PAGE of each fraction. Arrow indicates BAP1 and BAP1(C91S).

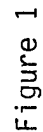
**Figure 5** BAP1 and BRCA1 interact *in vitro*. A) The GST, GST-hBAP1(483-729) and GST-hBAP1(483-594) fusion proteins were expressed and purified as described in Materials and Methods. Each lane represents the protein from 20  $\mu$ L of a 50:50 resin slurry separated by SDS-PAGE and visualized by Coomassie blue staining. B) BRCA1 and GST-hBAP1(483-729) interact *in vitro*. The Glutathione-Sepharose resins containing the proteins shown in Figure 5A were incubated in batch with *in vitro* -expressed, <sup>35</sup>S-labeled, BRCA1. After extensive washing, the proteins which remained bound were analyzed by SDS-PAGE and fluorography. Lane 1, Input, 2% of the labeled BRCA1 used in the associations with the glutathione resins. Lane 2, molecular weight markers. Lane 3, proteins bound to GST alone. Lane 4, proteins bound to GST-hBAP1(483-729). Lane 5, proteins bound to GST-hBAP1(483-594), a fusion protein lacking the BRCA1 interaction domain. Arrow indicates the BRCA1 protein. C) LexA-BRCA1-RF and GST-hBAP1(483-729) interact *in vitro*. Glutathione-Sepharose resins containing the GST or GST-hBAP1(483-729) proteins were incubated in batch with *in vitro* -expressed, <sup>35</sup>S-labeled, LexA-BRCA1-RF. After extensive washing, the proteins which remained bound were analyzed by SDS-PAGE and fluorography. Lane 1, proteins bound to GST alone. Lane 2, proteins bound to GST-hBAP1(483-729). Lane 3, Input, 5% of the labeled LexA-BRCA1-RF used in the associations with the glutathione resins. Bracket indicates the LexA-BRCA1-RF protein.

**Figure 6** Tissue expression and subcellular localization of BAP1. A) Multiple tissue northern blots were obtained from Clontech (Palo Alto, CA) and contain RNA from the indicated tissues. The blots were probed with the hBAP1(483-729) cDNA (nucleotides 1488 to 3525) as described by the manufacturer. Blots were also subsequently probed with a muscle actin cDNA. B) BAP1 is a nuclear protein. Detection of BAP1 by confocal microscopy in Hep2 cells transfected with the BAP1 cDNA. Cells were stained with  $\alpha$ BAP1 antibody as described in Materials and Methods.

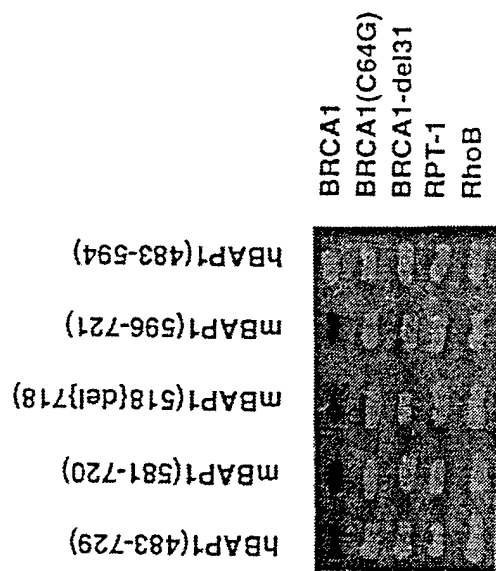
**Figure 7** BAP1 enhances BRCA1-mediated growth suppression. A) MCF7 cells were co-transfected with each of the plasmid constructs shown. Cells were then harvested and  $5 \times 10^5$  cells were plated in duplicate into G418-containing medium. Twenty one to 28 days later, cells were stained and colonies counted. The experiment was repeated 4 times with similar results. B) Quantitation of the results from (A).

**Figure 8** BAP1 maps to Chromosome 3p21.3. Fluorescent *In Situ* Hybridization (FISH) of partial metaphases using biotin-labeled BAP1 cDNA. A) the specific FISH signals on chromosome 3 (arrows), with B) the simultaneously BAPI-stained chromosomes, and C) a chromosome ideogram with the localization of BAP1 based on the DAPI-band pattern and FLpter value. The horizontal box indicates the variation in FLpter values on individual chromosomes.

**Figure 9** Mutational analysis of lung carcinomas. A) Southern blot hybridization with BamH1 digestion showing four distinct bands at 7.5kb, 4.0kb, 3.0kb, and 2.4kb detected by a full-length BAP1 probe. The non-small cell lung cancer NCI-H226 line shows an absence of the 7.5kb, 4.0kb, and 3.0kb bands. An aberrant 2.6kb band is detected in the H226 cell line. B) Northern blot hybridization showing a 4kb message which is absent in H226 and non-small cell lung cancer NCI-H1466 line. A fainter (5.0 kb) band is visible corresponding to cross hybridization with the 28S ribosomal component. C) SSCP analysis showing a homozygous shift in H1466 detected by RT-PCR amplification with primer set F (see text for primer sequences). Automated sequencing revealed an 8 base pair frameshift deletion in the H1466 cDNA, predicted to encode a 393 amino acid protein.



A.



B.

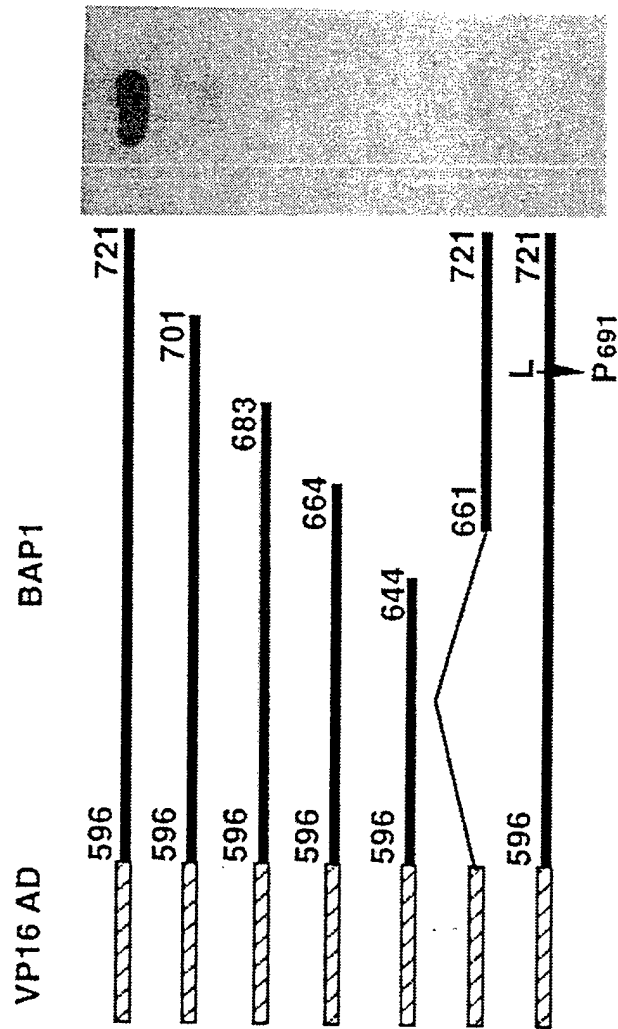


Figure 2

A.

## BAP1

1	GGCAC GAGGC ATGGC GCTGA GGGGC CGCCC CGCGG GAAG															
40	ATG	AAT	AAG	GGC	TGG	CTG	GAG	CTG	GAG	AGC	GAC	CCA	GGC	CTC	TTC	ACC
1	M	N	K	G	W	L	E	L	E	S	D	P	G	L	F	T
88	CTG	CTC	GTG	GAA	GAT	TTC	GGT	GTC	AAG	GGG	GTG	CAA	GTG	GAG	GAG	ATC
17	L	L	V	E	D	F	G	V	K	G	V	Q	V	E	E	I
136	TAC	GAC	CTT	CAG	AGC	AAA	TGT	CAG	GGC	CCT	GTA	TAT	GGA	TTT	ATC	TTC
33	Y	D	L	Q	S	K	C	Q	G	P	V	Y	G	F	I	F
184	CTG	TTC	AAA	TGG	ATC	GAA	GAG	CGC	CGG	TCC	CGG	CGA	AAG	GTC	TCT	ACC
49	L	F	K	W	I	E	E	R	R	S	R	R	K	V	S	T
232	TTG	GTG	GAT	GAT	ACG	TCC	GTG	ATT	GAT	GAT	GAT	ATT	GTG	AAT	AAC	ATG
65	L	V	D	D	T	S	V	I	D	D	D	I	V	N	N	M
280	TTC	TTT	GCC	CAC	CAG	CTG	ATA	CCC	AAC	TCT	TGT	GCA	ACT	CAT	GCC	TTG
81	F	F	A	H	Q	L	I	P	N	S	C	A	T	H	A	L
328	CTG	AGC	GTG	CTC	CTG	AAC	TGC	AGC	AGC	GTG	GAC	CTG	GGA	CCC	ACC	CTG
97	L	S	V	L	L	N	C	S	S	V	D	L	G	P	T	L
376	AGT	CGC	ATG	AAG	GAC	TTC	ACC	AAG	GGT	TTC	AGC	CCT	GAG	AGC	AAA	GGA
113	S	R	M	K	D	F	T	K	G	F	S	P	E	S	K	G
424	TAT	GCG	ATT	GGC	AAT	GCC	CCG	GAG	TTG	GCC	AAG	GCC	CAT	AAT	AGC	CAT
129	Y	A	I	G	N	A	P	E	L	A	K	A	H	N	S	H
472	GCC	AGG	CCC	GAG	CCA	CGC	CAC	CTC	CCT	GAG	AAG	CAG	AAT	GGC	CTT	AGT
145	A	R	P	E	P	R	H	L	P	E	K	Q	N	G	L	S
520	GCA	GTG	CGG	ACC	ATG	GAG	GCG	TTC	CAC	TTT	GTC	AGC	TAT	GTG	CCT	ATC
161	A	V	R	T	M	E	A	F	H	F	V	S	Y	V	P	I
568	ACA	GGC	CGG	CTC	TTT	GAG	CTG	GAT	GGG	CTG	AAG	GTC	TAC	CCC	ATT	GAC
177	T	G	R	L	F	E	L	D	G	L	K	V	Y	P	I	D
616	CAT	GGG	CCC	TGG	GGG	GAG	GAC	GAG	GAG	TGG	ACA	GAC	AAG	GCC	CGG	CGG
193	H	G	P	W	G	E	D	E	E	W	T	D	K	A	R	R
664	GTC	ATC	ATG	GAG	CGT	ATC	GGC	CTC	GCC	ACT	GCA	GGG	GAG	CCC	TAC	CAC
209	V	I	M	E	R	I	G	L	A	T	A	G	E	P	Y	H
712	GAC	ATC	CGC	TTC	AAC	CTG	ATG	GCA	GTG	GTG	CCC	GAC	CGC	AGG	ATC	AAG
225	D	I	R	F	N	L	M	A	V	V	P	D	R	R	I	K
760	TAT	GAG	GCC	AGG	CTG	CAT	GTG	CTG	AAG	GTG	AAC	CGT	CAG	ACA	GTA	CTA
241	Y	E	A	R	L	H	V	L	K	V	N	R	Q	T	V	L
808	GAG	GCT	CTG	CAG	CAG	CTG	ATA	AGA	GTA	ACA	CAG	CCA	GAG	CTG	ATT	CAG
257	E	A	L	Q	Q	L	I	R	V	T	Q	P	E	L	I	Q
856	ACC	CAC	AAG	TCT	CAA	GAG	TCA	CAG	CTG	CCT	GAG	GAG	TCC	AAG	TCA	GCC
273	T	H	K	S	Q	E	S	Q	L	P	E	E	S	K	S	A
904	AGC	AAC	AAG	TCC	CCG	CTG	GTG	CTG	GAA	GCA	AAC	AGG	GCC	CCT	GCA	GCC
289	S	N	K	S	P	L	V	L	E	A	N	R	A	P	A	A
952	TCT	GAG	GGC	AAC	CAC	ACA	GAT	GGT	GCA	GAG	GAG	GCG	GCT	GGT	TCA	TGC
305	S	E	G	N	H	T	D	G	A	E	E	A	A	G	S	C
1000	GCA	CAA	GCC	CCA	TCC	CAC	AGC	CCT	CCC	AAC	AAA	CCC	AAG	CTA	GTG	GTG
321	A	Q	A	P	S	H	S	P	P	N	K	P	K	L	V	V
1048	AAG	CCT	CCA	GGC	AGC	AGC	CTC	AAT	GGG	GTT	CAC	CCC	AAC	CCC	ACT	CCC
337	K	P	P	G	S	S	L	N	G	V	H	P	N	P	T	P
1096	ATT	GTC	CAG	CGG	CTG	CCG	GCC	TTT	CTA	GAC	AAT	CAC	AAT	TAT	GCC	AAG
353	I	V	Q	R	L	P	A	F	L	D	N	H	N	Y	A	K
1144	TCC	CCC	ATG	CAG	GAG	GAA	GAA	GAC	CTG	GCG	GCA	GGT	GTG	GGC	CGC	AGC
369	S	P	M	Q	E	E	E	D	L	A	A	G	V	G	R	S
1192	CGA	GTT	CCA	GTC	CGC	CCA	CCC	CAG	CAG	TAC	TCA	GAT	GAT	GAG	GAT	GAC
385	R	V	P	V	R	P	P	Q	Q	Y	S	D	D	E	D	D
1240	TAT	GAG	GAT	GAC	GAG	GAG	GAT	GAC	GTG	CAG	AAC	ACC	AAC	TCT	GCC	CTT
401	Y	E	D	D	E	E	D	D	V	Q	N	T	N	S	A	L
1288	AGG	TAT	AAG	GGG	AAG	GGA	ACA	GGG	AAG	CCA	GGG	GCA	TTG	AGC	GGT	TCT
417	R	Y	K	G	K	G	T	G	K	P	G	A	L	S	G	S
1336	GCT	GAT	GGG	CAA	CTG	TCA	GTG	CTG	CAG	CCC	AAC	ACC	ATC	AAC	GTC	TTG
433	A	D	G	Q	L	S	V	L	Q	P	N	T	I	N	V	L
1384	GCT	GAG	AAG	CTC	AAA	GAG	TCC	CAG	AAG	GAC	CTC	TCA	ATT	CCT	CTG	TCC
449	A	E	K	L	K	E	S	Q	K	D	L	S	I	P	L	S
1432	ATC	AAG	ACT	AGC	AGC	GGG	GCT	GGG	AGT	CCG	GCT	GTG	GCA	GTG	CCC	ACA
465	I	K	T	S	S	G	A	G	S	P	A	V	A	V	P	T
1480	CAC	TCG	CAG	CCC	TCA	CCC	ACC	CCC	AGC	AAT	GAG	AGT	ACA	GAC	ACG	GCC
481	H	S	Q	P	S	P	T	P	S	N	E	S	T	D	T	A
1528	TCT	GAG	ATC	GGC	AGT	GCT	TTC	AAC	TCG	CCA	CTG	CGC	TCG	CCT	ATC	CGC
497	S	E	I	G	S	A	F	N	S	P	L	R	S	P	I	R

Figure 3A



1576	TCA	GCC	AAC	CCG	ACG	CGG	CCC	TCC	AGC	CCT	GTC	ACC	TCC	CAC	ATC	TCC
513	S	A	N	P	T	R	P	S	S	P	V	T	S	H	I	S
1624	AAG	GTG	CTT	TTT	GGA	GAG	GAT	GAC	AGC	CTG	CTG	CGT	GTT	GAC	TGC	ATA
529	K	V	L	F	G	E	D	D	S	L	L	R	V	D	C	I
1672	CGC	TAC	AAC	CGT	GCT	GTC	CGT	GAT	CTG	GGT	CCT	GTC	ATC	AGC	ACA	GGC
545	R	Y	N	R	A	V	R	D	L	G	P	V	I	S	T	G
1720	CTG	CTG	CAC	CTG	GCT	GAG	GAT	GGG	GTG	CTG	AGT	CCC	CTG	GCG	CTG	ACA
561	L	L	H	L	A	E	D	G	V	L	S	P	L	A	L	T
1768	GAG	GGT	GGG	AAG	GGT	TCC	TCG	CCC	TCC	ATC	AGA	CCA	ATC	CAA	GGC	AGC
577	E	G	G	K	G	S	S	P	S	I	R	P	I	O	G	S
1816	CAG	GGG	TCC	AGC	AGC	CCA	GTG	GAG	AAG	GAG	GTC	GTG	GAA	GCC	ACG	GAC
593	O	G	S	S	S	P	V	E	K	E	V	V	E	A	T	D
1864	AGC	AGA	GAG	AAG	ACG	GGG	ATG	GTG	AGG	CCT	GGC	GAG	CCC	TTG	AGT	GGG
609	S	R	E	K	T	G	M	V	R	P	G	E	P	L	S	G
1912	GAG	AAA	TAC	TCA	CCC	AAG	GAG	CTG	CTG	GCA	CTG	CTG	AAG	TGT	GTG	GAG
625	E	K	Y	S	P	K	E	L	L	A	L	L	K	C	V	E
1960	GCT	GAG	ATT	GCA	AAC	TAT	GAG	GCG	TGC	CTC	AAG	GAG	GAG	GTA	GAG	AAG
641	A	E	I	A	N	Y	E	A	C	L	K	E	E	V	E	K
2008	AGG	AAG	AAG	TTC	AAG	ATT	GAT	GAC	CAG	AGA	AGG	ACC	CAC	AAC	TAC	GAT
657	R	K	K	F	K	I	D	D	Q	R	R	T	H	N	Y	D
2056	GAG	TTC	ATC	TGC	ACC	TTT	ATC	TCC	ATG	CTG	GCT	CAG	GAA	GGC	ATG	CTG
673	E	F	I	C	T	F	I	S	M	L	A	Q	E	G	M	L
2104	GCC	AAC	CTA	GTG	GAG	CAG	AAC	ATC	TCC	GTG	CGG	CGG	CGC	CAA	GGG	GTC
689	A	N	L	V	E	Q	N	I	S	V	R	R	R	Q	G	V
2152	AGC	ATC	GGC	CGG	CTC	CAC	AAG	CAG	CGG	AAG	CCT	GAC	CGG	CGG	AAA	CGC
705	S	I	G	R	L	H	K	Q	R	TGA	P	D	R	R	K	R
2200	TCT	CGC	CCC	TAC	AAG	GCC	AAG	CGC	CAG	TGA						
721	S	R	P	Y	K	A	K	R	Q	*						

2230	GGACT	GCTGG	CCCTG	ACTCT	GCAGC	CCACT	CTTGC	CGTGT	GGCCC	TCACC	AGGGT
2285	CCTTC	CCTGC	CCCAC	TTCCC	CTTTT	CCCAG	TATTA	CTGAA	TAGTC	CCAGC	TGGAG
2340	AGTCC	AGGCC	CTGGG	AATGG	GAGGA	ACCAG	GCCAC	ATTCC	TTCCA	TCGTG	CCCTG
2395	AGGCC	TGACA	CGGCA	GATCA	GCCCC	ATAGT	GCTCA	GGAGG	CAGCA	TCTGG	AGTTG
2450	GGGCA	CAGCG	AGGTA	CTGCA	GCTTC	CTCCA	CAGCC	GGCTG	TGGAG	CAGCA	GGACC
2505	TGGCC	CTTCT	GCCTG	GGCAG	CAGAA	TATAT	ATTTT	ACCTA	TCAGA	GACAT	CTATT
2560	TTTCT	GGGCT	CCAAC	CCAAC	ATGCC	ACCAT	GTTGA	CATAA	GTTCC	TACCT	GACTA
2615	TGCTT	TCTCT	CCTAG	GAGCT	GTCCT	GGTGG	GCCCA	GGTCC	TTGTA	TCATG	CCACG
2670	GTCCC	AACTA	CAGGG	TCCTA	GCTGG	GGGCC	TGGGT	GGGCC	CTGGG	CTCTG	GGCCC
2725	TGCTG	CTCTA	GCCCC	AGCCA	CCAGC	CTGTC	CCTGT	TGTAA	GGAAG	CCAGG	TCTTC
2780	TCTCT	TCATT	CCTCT	TAGGA	GAGTG	CCAAA	CTCAG	GGACC	CAGCA	CTGGG	CTGGG
2835	TTGGG	AGTAG	GGTGT	CCCAG	TGGGG	TTGGG	GTGAG	CAGGC	TGCTG	GGATC	CCATG
2890	GCCTG	AGCAG	AGCAT	GTGGG	AACTG	TTCAG	TGGCC	TGTGA	ACTGT	CTTCC	TTGTT
2945	CTAGC	CAGGC	TGTTT	AAGAC	TGCTC	TCCAT	AGCAA	GGTTC	TAGGG	CTCTT	CGCCT
3000	TCAGT	GTTGT	GGCCC	TAGCT	ATGGG	CCTAA	ATTGG	GCTCT	AGGTC	TCTGT	CCCTG
3055	GCGCT	TGAGG	CTCAG	AAGAG	CCTCT	GTCCA	GCCCC	TCAGT	ATTAC	CATGT	CTCCC
3110	TCTCA	GGGGT	AGCAG	AGACA	GGGTT	GCTTA	TAGGA	AGCTG	GCACC	ACTCA	GCTCT
3165	TCCTG	CTACT	CCAGT	TTCCT	CAGCC	TCTGC	AAGGC	ACTCA	GGGTG	GGGGA	CAGCA
3220	GGATC	AAGAC	AACCC	GTTGG	AGCCC	CTGTG	TTCCA	GAGGA	CCTGA	TGCCA	AGGGG
3275	TAATG	GGCCC	AGCAG	TGCCT	CTGGA	GCCCC	GGCCC	CAACA	CAGCC	CCATG	GCCTC
3330	TGCCA	GATGG	CTTTG	AAAAA	GGTGA	TCCAA	GCAGG	CCCCT	TTATC	TGTAC	ATAGT
3385	GACTG	AGTGG	GGGGT	GCTGG	CAAGT	GTGGC	AGCTG	CCTCT	GGGCT	GAGCA	CAGCT
3440	TGACC	CCTCT	AGCCC	CTGTA	AATAC	TGGAT	CAATG	AATGA	ATAAA	ACTCT	CCTAA
3495	GAATC	TCCTG	AGAAA	AAAAA	AAAAA	AAAAA	G				

**B.**

BAP1	1	- - - - -	MNKGWLELE	<b>E</b>	S	D	P	G	L	F	T	L	L	V	E	D	F	<b>G</b>	V	K	G	-	V	Q	V	E	E	I	Y	D	<b>L</b>	Q	S	- -	37													
CAEEL-c08811.7	1	M	G	K	K	I	M	T	D	A	G	S	W	C	L	I	<b>E</b>	S	D	P	G	V	F	T	E	M	L	R	G	F	<b>G</b>	V	D	G	-	L	Q	V	E	E	L	Y	S	<b>L</b>	D	D	-	44
UCH-DROME	1	- - - - -	MLTWTPL	<b>E</b>	S	N	P	E	V	L	T	K	Y	I	H	K	L	A	V	S	P	A	W	S	V	T	D	V	I	G	L	E	D	-	D	38												
YUH1	1	- - - -	MSGENRAVVP	<b>E</b>	S	N	P	E	V	F	T	N	F	A	H	K	L	<b>G</b>	L	K	N	E	W	A	Y	F	D	I	Y	S	<b>L</b>	T	E	P	E	43												
UCH-L3	1	- - - - -	MEGQRWLPL	<b>E</b>	A	N	P	E	V	T	N	Q	F	L	K	Q	L	<b>G</b>	L	H	P	N	W	Q	F	V	D	V	Y	G	M	D	P	-	E	40												
UCH-L1	1	- - - - -	MQLKPM	<b>E</b>	I	N	P	E	M	L	N	K	V	L	S	R	L	<b>G</b>	V	A	G	Q	W	R	F	V	D	V	L	G	<b>L</b>	E	E	-	E	37												

BAP1	38	KC---	QGPVYGFIF	LFK	WIEERRSR	RRKVSTL	VDDTSV	IDD	DDI	VNNMF	81
CAEEL-C08811.7	45	-DKAMTR	PPTYGLIF	LFK	WRQGDE---	TTGIP---	---	---	---	SDKQNI	78
UCH-DROME	39	TLEWIPR	PVKAFIL	LFPC	SETYEKHR-	TEEH	DRIKE	VEEQ	HPED	LF	83
YUH1	44	LLAFLPR	PVKAIVL	LFPI	NEDRKSST-	SQQIT-	---	---	---	SSYDVI	80
UCH-L3	41	LLSMVPR	PVCAVLL	LFPI	TEKYEVFR-	TEEE	EKIKS	QQQ	DVTSS	VY	85
UCH-L1	38	SLGSVPAP	ACALLL	LFPL	TAQHENFR-	KKQIEELK-	GQEV	SPKVY		80	

BAP1	82	FAH	Q	L	I	P	N	S	C	A	T	H	A	L	L	S	V	L	L	N	C	S	S	-	-	V	D	-	L	G	P	T	L	S	R	M	K	D	F	T	K	G	F	S	P	-	124
CAEEL-C08B11.7	79	FAH	Q	T	I	Q	N	A	C	A	T	Q	A	L	I	N	L	M	N	V	E	D	-	T	D	V	K	L	G	N	I	L	N	Q	Y	K	E	F	A	I	D	L	P	-	123		
UCH-DROME	84	YMR	Q	F	T	H	N	A	C	G	T	V	A	L	I	H	S	V	A	N	N	K	E	-	V	D	I	D	R	G	-	V	L	K	D	F	L	E	K	T	A	S	L	P	-	127	
YUH1	81	WFK	Q	S	V	K	N	A	C	G	L	Y	A	I	L	H	S	L	S	N	N	Q	S	-	-	L	L	E	P	G	S	D	L	D	N	F	L	K	S	Q	S	D	T	S	S	-	125
UCH-L3	86	FMK	Q	T	I	S	N	A	C	G	T	I	G	L	I	H	A	I	A	N	N	K	D	K	M	H	F	E	S	G	S	T	L	K	K	F	L	E	E	S	V	S	M	S	P	-	131
UCH-L1	81	FMK	Q	T	I	G	N	S	C	G	T	I	G	L	I	H	A	V	A	N	N	Q	D	K	L	G	F	E	D	G	S	V	L	K	Q	F	L	S	E	T	E	K	M	S	P	-	126

BAP1	125	ESKGYAIGNAPELAKA	H	NSHARPEPRHLPEK	Q	NGLSAVRTMEAF	H	FV	171
CAEEL-c08811.7	124	NTRGHCLSNSEEIRTV	H	NSFSR	- - - - QTLF	ELD	IKGGESE	DNYH	FV
UCH-DROME	128	EERGRALEKDEKFTAD	H	EALAQ	- - - - - EG	Q	-TNAANHEKVI	H	F
YUH1	126	KNRFDDVTTDQFVLNV	I	KENVQT	- - - - FSTG	Q	SEAPEATADTNL	H	Y
UCH-L3	132	EERARYLENYDAIRVT	H	ETSAH	- - - - - EG	Q	TEAPSIDEKVDL	H	F
UCH-L1	127	EDRAKCFEKNEAIAAA	H	DAVAQ	- - - - - EG	Q	- - CR - VDDKVN	H	F

BAP1	172	SYVPIT	G	R	L	F	E	L	D	G	L	-	K	V	Y	P	I	D	H	G	-	-	-	P	W	G	E	D	E	E	W	T	D	K	A	R	R	V	I	M	E	R	I	214
CAEEL-c0881.7	166	TYVPI	G	N	K	V	E	L	D	G	L	-	R	E	L	P	L	E	V	A	-	-	-	E	F	Q	K	E	Q	D	W	I	E	A	I	K	P	V	I	Q	R	M	208	
UCH-DROME	167	ALVNKE	G	T	L	Y	E	L	D	G	R	-	K	S	F	P	I	K	H	G	-	-	-	P	T	S	E	E	-	T	F	V	K	D	A	A	K	V	C	K	E	F	M	208
YUH1	169	TYVEENG	G	G	I	F	E	L	D	G	R	N	L	S	G	P	L	Y	L	G	K	S	D	P	T	A	T	D	-	L	I	E	Q	E	L	V	R	V	R	V	A	S	Y	214
UCH-L3	172	ALVHVD	G	H	L	Y	E	L	D	G	R	-	K	P	F	P	I	N	H	G	-	-	-	E	T	S	D	E	-	T	L	L	E	D	A	I	E	V	C	K	K	F	M	213
UCH-L1	164	LFNNVD	G	H	L	Y	E	L	D	G	R	-	M	P	F	P	V	N	H	G	-	-	-	A	S	S	E	D	-	T	L	L	K	D	A	A	K	V	C	R	E	F	T	205

BAP1	215	GLATAGE	E	PYHDIRFNLMAVVPDRRIKYEARLHV LKVNRQTVLEALQQ	261
CAEEL- <sup>c08B11.7</sup>	209	QKYSEGE	- - - I	T F N L M A L V P N R K Q K L Q E M M E N L I Q A N E N N E L E E Q I	251
UCH-DROME	209	ARD-PNE	- - - V	R F T V L A L T A A Q Q	227
YUH1	215	MEN-ANEED-VLNFA	M L G	L G P N W E	236
UCH-L3	214	ERD-PDE	- - - L	R F N A I A L S A A	230
UCH-L1	206	ERE-QGE	- - - V	R F S A V A L C K A A	223

BAP1 630 K E L L A L L K C V E A E I A N Y E A C L K E E V E K R K K F K I D 633  
 CAEL-C08B11.7 238 L I Q A N E N N E L E E Q I A D L N K A I A D E D Y K M E M Y R K E 271

BAP1 634 D Q R R T H N Y D E F I C T F I S M L A Q E G M L A N L V E Q N I S 667  
CAEEL-C08B11.7 272 N N R R R H N Y T P F V I E L M K I L A K E G K L V G L V D N A Y Q 305

BAP1 668 V R R R Q G V S I G R L H K Q R K P D R R K R S R P Y K A K R Q 729  
CAEEL-C08B11.7 306 A A K - E K - S - - K L N T D I T K L E L K R K Q 326

Figure 3B

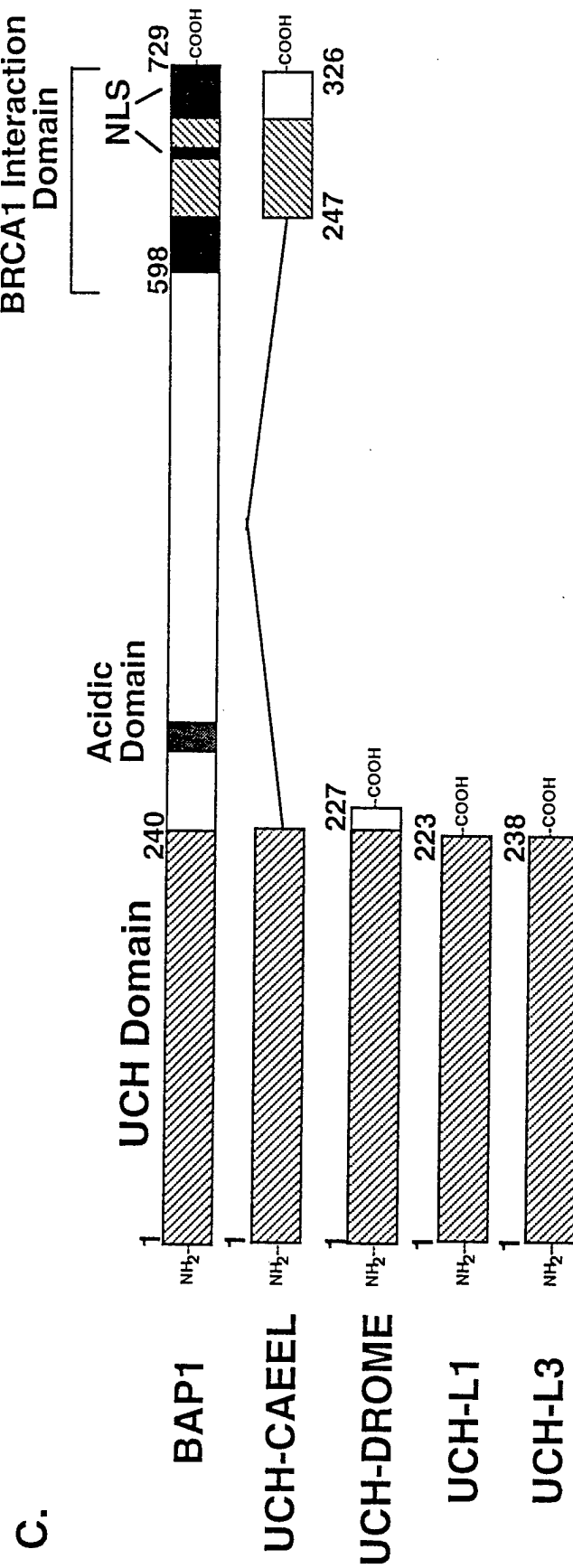


Figure 3C



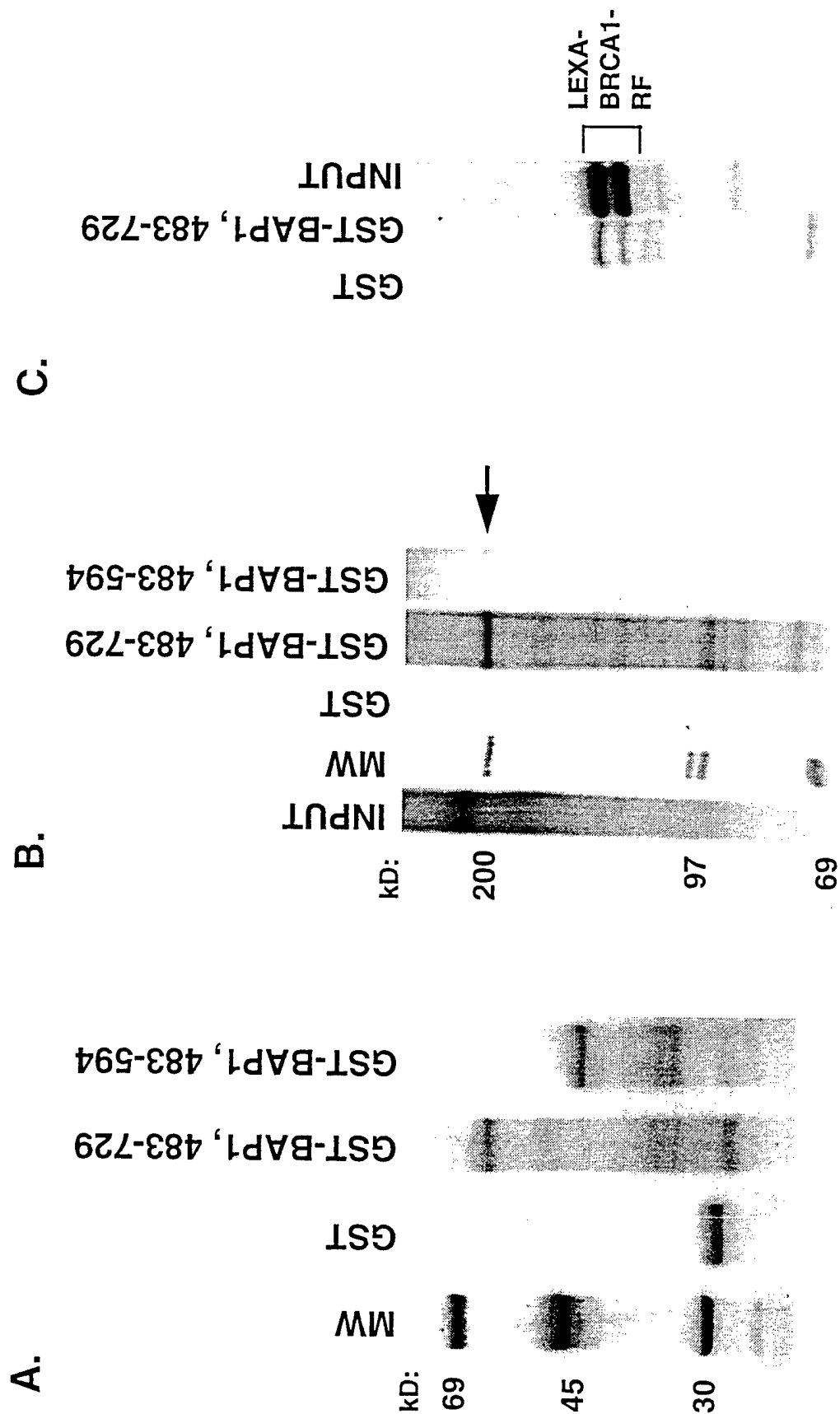


Figure 5

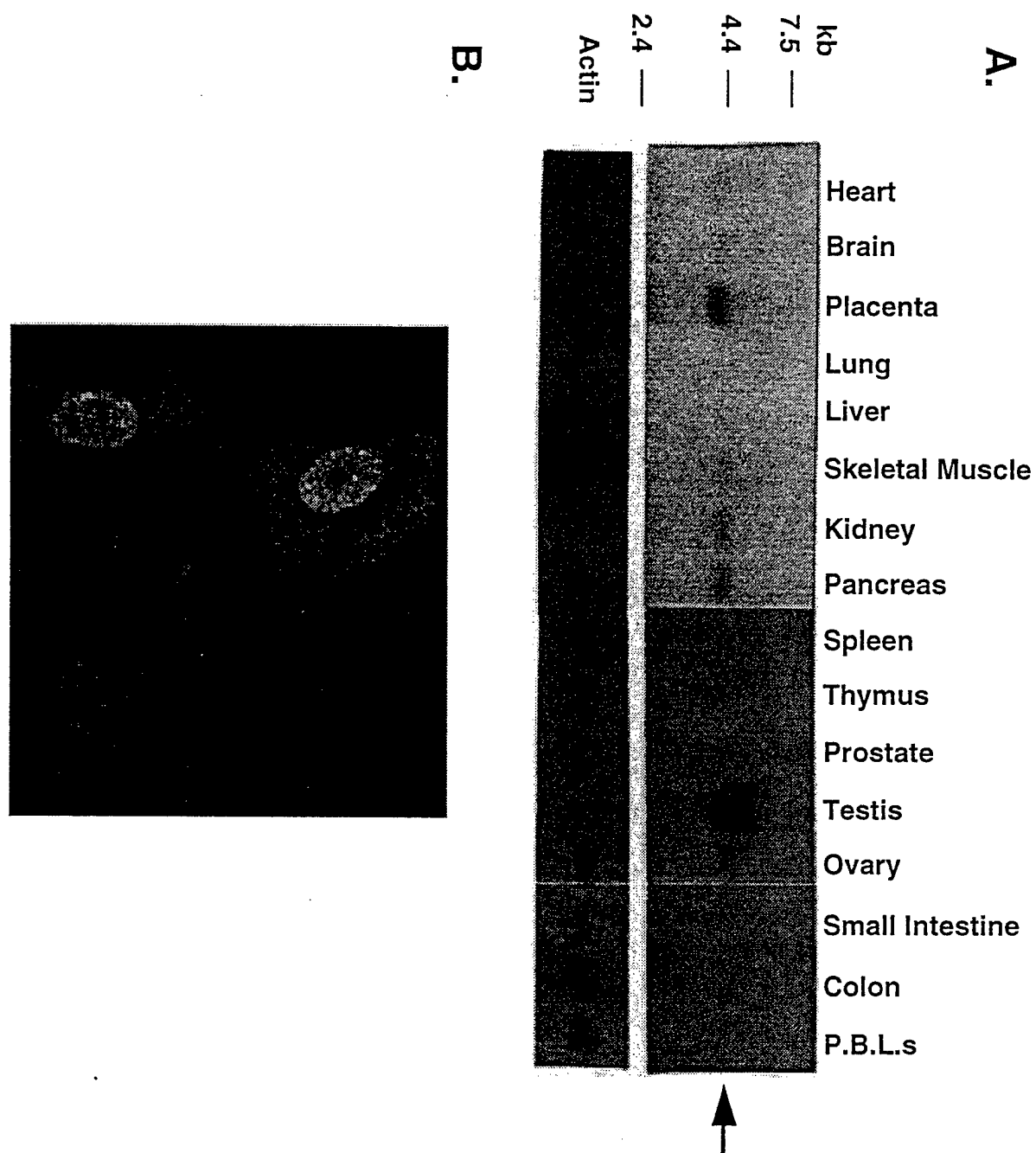


Figure 6

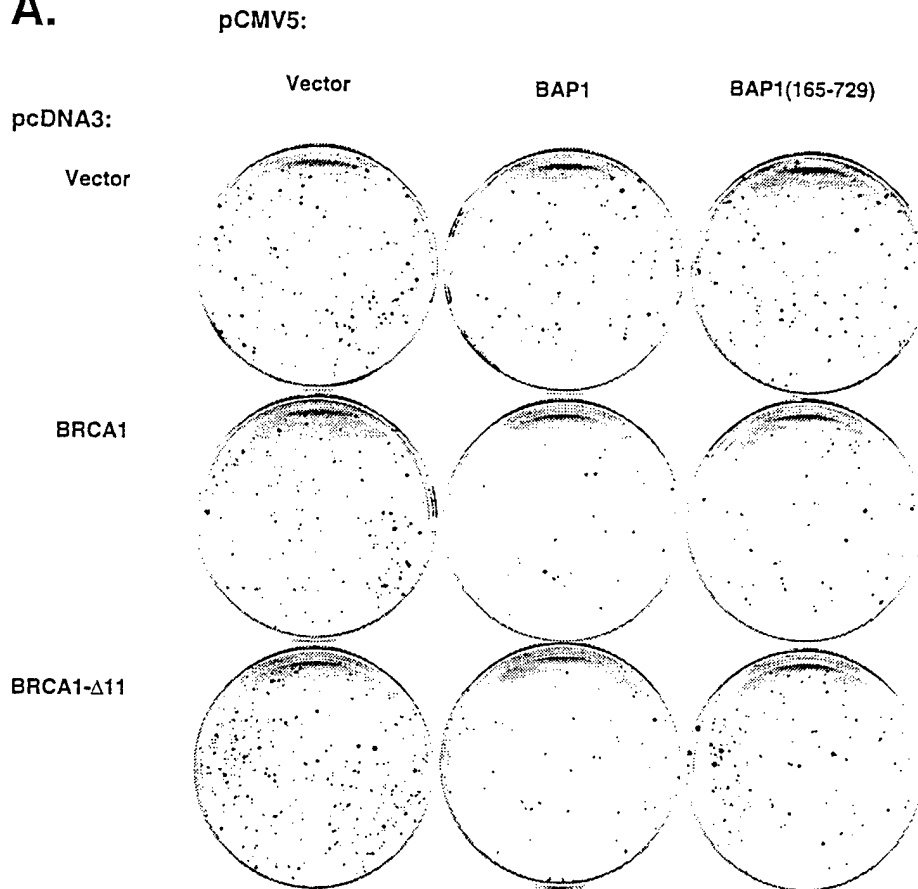
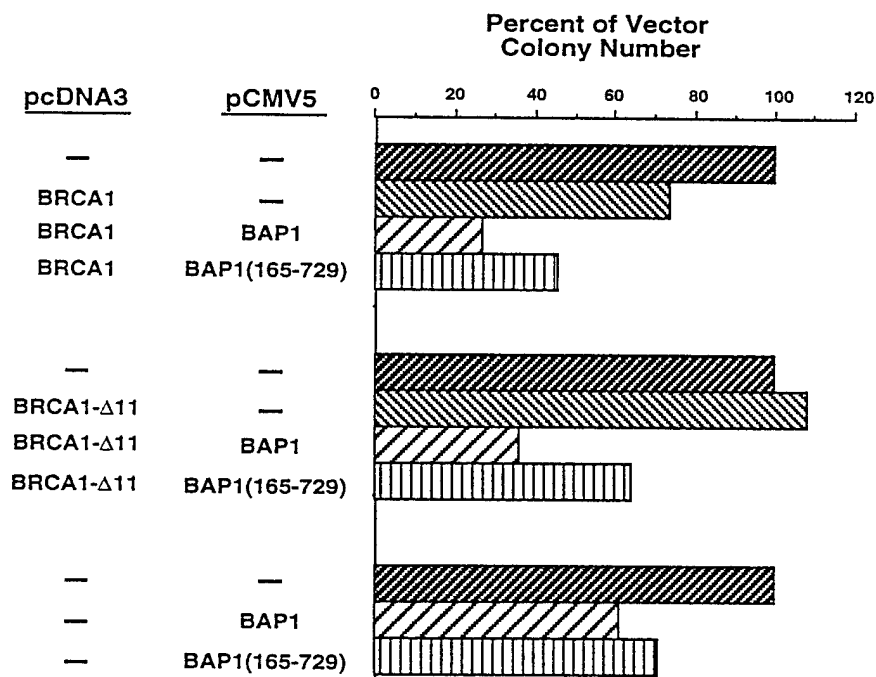
**A.****B.**

Figure 7

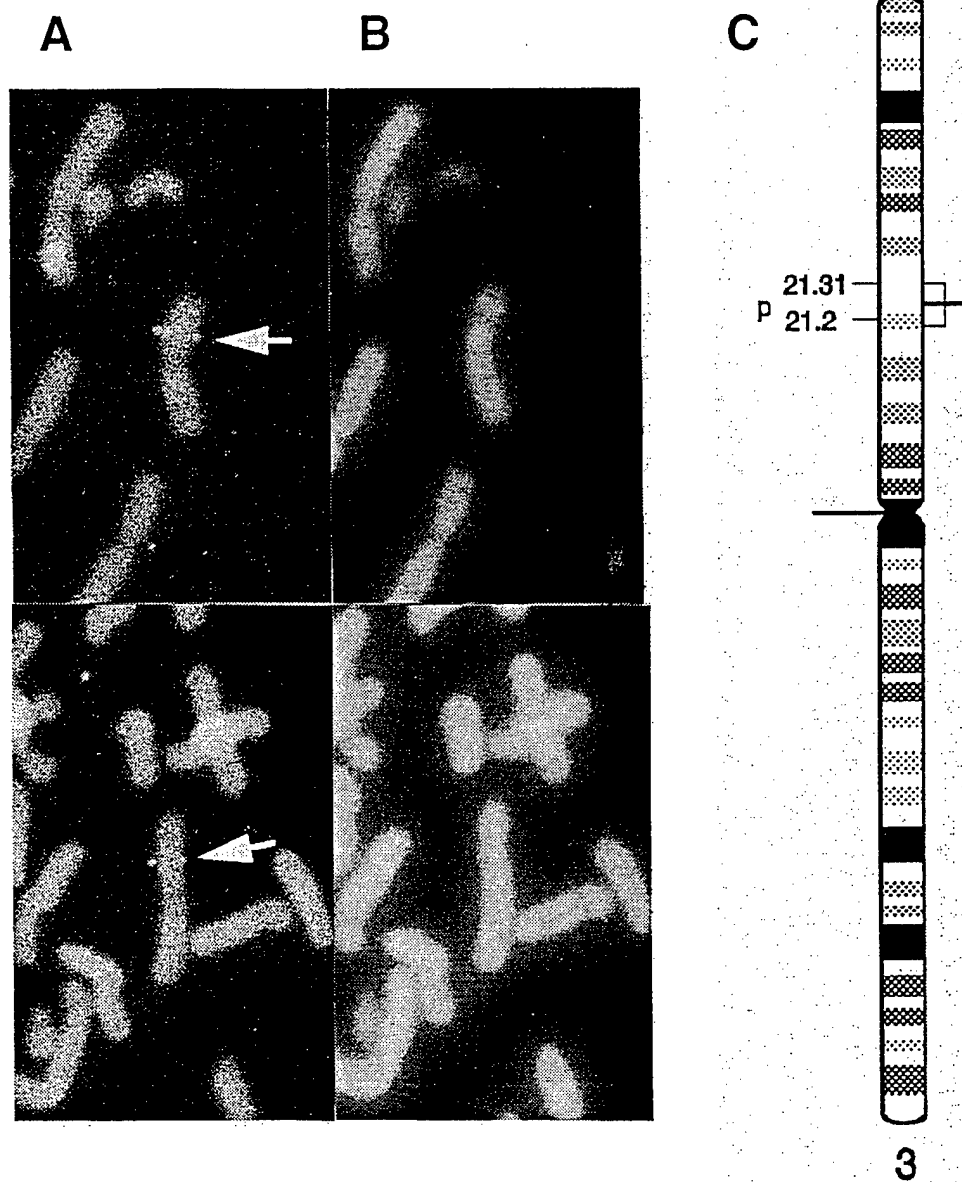
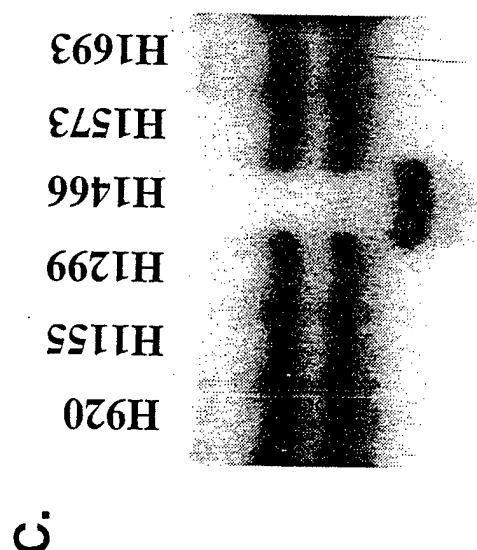
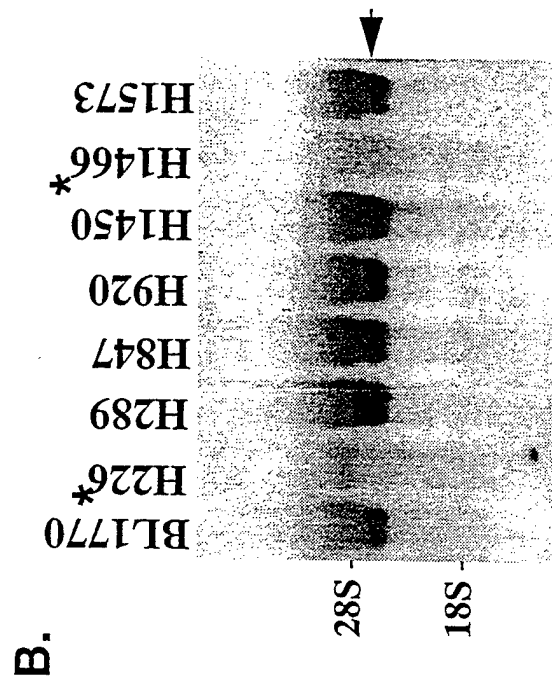
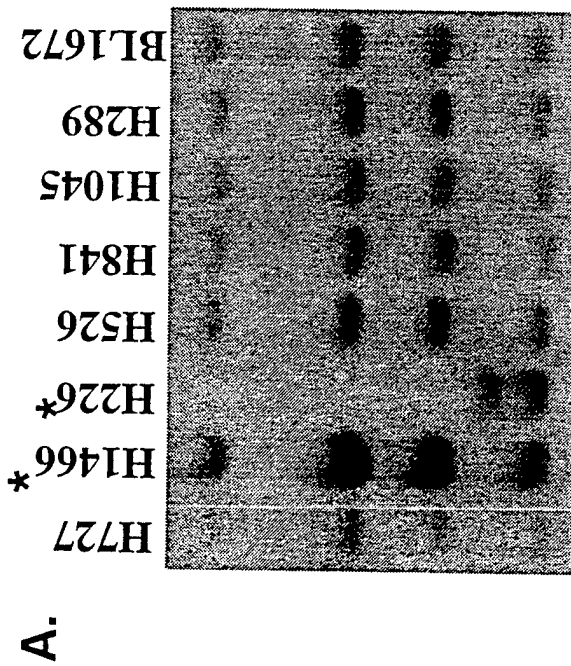


Figure 8





Normal:  
5'...GGC CGC AGC CGA GTT CCA GTC..3'  
... G R S R V P V .... 729aa

H1466: 1198-1205 del CGAGTTCC  
5'...GGC CGC AGC------(del)-----AGT..3'  
... G R S S ..... 393aa

Figure 9